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Functional DNA: A Powerful Argument for Design

by Eric P.

The concept of junk DNA has garnered renewed attention in Intelligent Design circles. On May 2nd, 2024, geologist and Discovery Institute fellow Casey Luskin debated Rutgers evolutionary biology professor and anti-creationist Dan Cardinale. Luskin summarizes his position:

> "While function for junk DNA may not, strictly speaking, refute evolution, the discovery of widespread functionality for non-coding or junk DNA represents a failed prediction for evolution... The evidence of mass functionality for junk DNA represents a spectacularly successful prediction of ID."[1]

Luskin is correct about the history of predictions, as I've written elsewhere.[2] However, contrary to Luskin's claims, Biblical creationists might be surprised to learn that the absence of junk DNA does indeed contradict evolutionary theory and shows that complex species could not have existed for millions of years. Given that Luskin believes life and the Earth are billions of years old, he may be unwilling to follow these implications.

Genetic Entropy

The arithmetic is simple. Each human child has about 70 new mutations, along with mutations inherited from their parents. Many large, complex animals likely have a similar mutation rate. If almost all of our DNA is junk, then these mutations are mostly changing letters of DNA that don't matter. But if more than a small percentage of DNA letters need a specific

sequence to function, then every offspring ends up with more harmful mutations than their parents.

Most harmful mutations have only very mild effects. That's good in the short term. But that also means natural selection usually can't filter them out. Seasoned creationists recognize this as the Genetic Entropy argument pioneered by geneticist John Sanford. Creationists Gibson, Baumgardner, Brewer, and Sanford used a computer simulation to model only 10 harmful mutations per generation and saw:

> …a steady decline in fitness that is not even halted by extremely intense selection pressure (12 offspring per female, 10 selectively removed)… under most realistic circumstances, the large majority of harmful mutations are essentially unaffected by natural selection and continue to accumulate unhindered… With a mutation rate of 10, almost half of all deleterious [harmful] mutations were retained, with a nearly constant accumulation rate of 4.5 mutations per individual per generation.[3]

Even many ardent anti-creationists recognize this problem of having too many mutations. Biochemist and textbook author Larry Moran states: "If the deleterious mutation rate is too high, the species will go extinct… It should be no more than 1 or 2 deleterious mutations per generation."[4]

If mutations drive species to extinction, they couldn't have been around for millions of years.

Defining Function

ENCODE is an ongoing research project by the United States National Institute of Health (NIH) to find function in human

See **DNA** *on page 4*

Math Matters

Spinning Seeds from the Sky

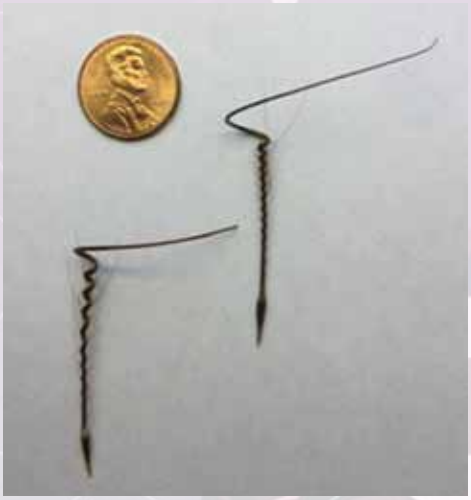
by Don DeYoung, PhD

There are many fascinating discoveries at the intersection of math and biomimicry. The latter term describes the discovery of practical designs in nature. For example, Velcro is based on the flexible hooks of cockleburs. This article extends biomimicry to a classic example of intelligent design—erodium or filaree, a genus of plant known by the corkscrew stem on its seeds. When a seed falls to the ground, the stem absorbs moisture and unwinds, pushing the seed downward and self-planting.

The geometric shape of the plant stem is called a spiral helix. This is similar to an auger or the DNA helix structure, except that the plant's spiral radius r increases along the stem. The equation for this "Archimedes spiral" is $r = c\Theta$ where c is a constant and the angle Θ is measured in radians. To observe erodium in action, I placed one of the pictured seeds in water and the stem unraveled over 15 minutes. I then warmed the seed to speed up the drying process and it rapidly rewound itself in just two minutes. There were ten turns total, so the drying seed stem turned at ~0.5 radians/second (30 degrees/second), which is impressive dynamic movement for a plant.

Design engineers have mimicked the self-drilling nature of erodium with an artificial seed carrier made from a thin wood shaving of white oak (Luo, 2023). Like the erodium seed stem, this wood is hygroscopic—curled when dry and straight when moist. When the device is placed on the ground, daily humidity changes will self-bury an attached seed or tree seedling. One commercial goal is to air-drop the devices in inaccessible areas for reforestation.

Significant study has been done on the mechanism of these self-planting seeds by Pandolfi and colleagues (2012). Although written from an evolutionary viewpoint, the mathematical analysis in their paper clearly describes how these plants are intelligently designed. The article also expresses the lofty goal of airborne seed dispersal on other solar system planets and moons.



Filaree seeds from Arizona. Note the hair-like spikes on the seed stems which give traction as the seeds are driven into soil by the twisting action. Photo by Don DeYoung.

Biomimicry provides countless examples of useful designs in nature which await our discovery and application. Added to the list is air-dropped, self-planting seeds.

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Table of Contents

Functional DNA: A Powerful Argument for Design . . 1

Math Matters 2

Research Matters. 3

Prayer Matters 8

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Summaries of Cutting-Edge Research from the *Creation Research Society Quarterly*

Summaries by Andrea Reitan

Crassostrea Oyster Fossils Show Evidence of Extreme Longevity

Bible skeptics often ridicule the claims in Scripture of pre-Flood people living for over 900 years and post-Flood people living over 400 years, eventually dropping to lifespans of 200 years and lower. Centuries-long lifespans are beyond present-day human experience. This should create an interest in creationists in possible corroboration from historical or paleontological data. Some corroboration has already been discussed among creationists regarding possible historical and cultural confirmations of extremely long lifespans, possible evidence of greater longevity in post-Flood Neanderthal fossils, and a possible connection between greater longevity and past giantism.

In the winter 2024 issue of *CRSQ*, Hebert, Overman, and Sherwin compare fossil *Crassostrea* oysters with their modern-day counterparts. *Crassostrea virginica*, a modern oyster, has been recorded as reaching lengths of up to 8-10 inches (20-25 cm) and ages of 20 years, but these are exceptional rather than the norm. However, *Crassostrea* fossils show that these oysters likely experienced much greater lifespans in the past, suggesting that humans were not the only creatures that lived longer before the Flood.

The authors explain that many animals exhibit a growth pattern in which their length reaches a maximum value as they mature, termed "skeletal maturity." Studies have shown that greater longevity is often positively correlated with reaching skeletal maturity at a later age. This is different from "sexual maturity," which is often reached earlier than skeletal maturity. The observation is that slower growth and later reproductive readiness are often related to greater longevity.

In Genesis 5:15 and 21, the patriarchs who were youngest when their sons were born were 65 years old. The sons recorded in the genealogies may not have all been firstborn, but some probably were. The authors say that it seems unlikely that the patriarchs were waiting 50+ years to begin sexual relations and have children after becoming sexually mature at 15 or 16 years old. They say it is more likely that pre-Flood people matured later than humans do today.

Some studies have found that bivalve mollusks exhibit a positive correlation between size and longevity, but others have not. Other animal groups have also been studied. Many of these studies looked at differences between Genesis kinds—at the taxonomic levels of class, order, and family. In creation science, there is more interest in the results within the Genesis kinds, but such studies are less abundant and show conflicting results.

Bivalve longevity is influenced by several factors such as temperature, salinity, water current velocity, food supply, and crowding. The authors explain that it is impossible to completely eliminate the influence of the various factors when comparing fossil and living species, but it can be minimized by studying populations geographically close to each other, even though separated by time. Both creationists and evolutionists would agree that fossil *Crassostrea* oysters lived at similar latitudes to extant species which are believed to be their direct descendants.

A comparison can be made between the fossil and modern *Crassostrea* oysters by counting the growth bands in their shells—a method called sclerochronology—similar to counting tree rings. Since creationists are generally distrustful of claims that dendrochronology can provide accurate timelines going back thousands of years, the authors address the question of whether the band counts can be trusted. They state that because *Crassostrea virginica* is important to the seafood industry, their modern lifespans have been directly observed, giving confidence that sclerochronological analysis can produce reasonably accurate inferred ages, especially since the analysis is not relying on "cross-matching" banding patterns from one group to another. Geochemical variations can also help identify seasonal patterns.

Another point of agreement between creationists and evolutionists is that the band counts probably underestimate the true ages of the bivalves being studied. One reason for this is that as the bivalves live longer, the bands become thinner and harder to see.

The evidence presented in this paper should encourage Bible-believing Christians that they can trust what the Scriptures say about human longevity both before and shortly after the Flood. While more in-depth analysis is required, there is evidence that extreme longevity was not limited to the human race.

Hebert, J., R. Overman, and F.J. Sherwin. 2024. *Crassostrea* Oyster Fossils Show Evidence of Extreme Longevity. *CRSQ 60*(3):171-190.

The Clay Consolidation Problem

The modern creationist movement is generally believed to have begun about sixty years ago with the publishing of *The Genesis Flood: The Biblical Record and Its Scientific Implications* by Whitcomb and Morris (1961). In that time, several

See **Summaries** *on page 7*

DNA

continued from page 1

DNA. The project involves hundreds of scientists and hundreds of millions of dollars in funding. In 2012 they eulogized the concept of junk DNA by announcing that at least 80% of human DNA has function. Evolutionists were not happy, and rightly noted that there are different ways to define function:

1. Sequence-specific function: DNA letters where function will be affected if they're changed.

2. Functional elements: Sequences of DNA letters that perform a specific function. Some of the DNA letters within them are sequence-specific functional while perhaps others could be swapped with no detectible effect on function. A popular example of a functional element is a gene that has instructions for making a protein.

Evolutionists correctly pointed out that ENCODE's 80% applied only to functional elements. But many incorrectly argued that the 80% estimate was too high. What does the data show?

How Much DNA is Functional Elements?

First, we'll look at how much DNA is within functional elements.

85% of DNA is transcribed

At least 85% of DNA in human cells, and probably more, is transcribed (copied) to a molecule called RNA. Some of the RNA serves as a messenger with instructions for making proteins. Most RNA has other functions. Researchers note:

> We found evidence that 85.2% of the genome is transcribed. This result closely agrees with [ENCODE's estimate of] transcription of 83.7% of the genome... even more read depth may reveal yet higher genomic coverage.[5]

DNA is copied to RNA in specific patterns

Human development involves a single fertilized egg cell dividing into trillions of cells to eventually produce an adult human. This includes differentiating into various types of bone, muscle, and nerve cells, among hundreds of others. Researchers see different cell types use different sections of DNA at different stages of development, in precise and reproducible patterns:

> [T]he vast majority of the mammalian genome is differentially transcribed in precise cell-specific patterns to produce large numbers of intergenic, interlacing, antisense and intronic non-protein-coding RNAs, which show dynamic regulation in embryonal development, tissue differentiation and disease…[6]

They go on to note this is best explained by the DNA being functional, but not by DNA accidentally getting copied to RNA as some evolutionists argue.

RNA is taken to specific locations

Among non-coding RNA produced in the human brain, about 80% are taken to specific locations within cells:

> In 80% of the cases where we had sufficient resolution to tell, these RNAs [in the human brain] are trafficked to specific subcellular locations. So this is not some fuzzy random signal: their expression is extremely precise, both in terms of the cell specificity and in terms of subcellular localization.[6]

This seems more compatible with function.

RNAs are usually functional when tested

If you take a survey of RNAs and find them functional, it's reasonable to assume most of the rest are functional too:

> [W]here tested, these noncoding RNAs usually show evidence of biological function in different developmental and disease contexts, with, by our estimate, hundreds of validated cases already published and many more en route, which is a big enough subset to draw broader conclusions about the likely functionality of the rest.[6]

This has led some genomicists to suspect that nearly 100% of the human genome will be found to be made of functional elements. The prestigious non-coding DNA researcher John Mattick writes:

> Most of the human genome — perhaps not unreasonably 99% — must be devoted to the regulation of development — generating ~30–40 trillion cells with highly specific arrangements, characteristics, and connections in an adult capable of reproduction and parenting.[7]

ENCODE lead researcher Ewan Birney states:

> It's likely that 80 percent [estimate of functional human DNA] will go to 100 percent. We don't really have any large chunks of redundant DNA. This metaphor of junk isn't that useful.[8]

How Much DNA is Sequence Specific?

If most DNA is composed of functional elements, how many new harmful mutations do each of us get per generation? It's not reasonable to assume only 1-2% of DNA letters within these functional elements will cause problems if changed.

From RNA structure

We know that "the nucleic acids that make up RNA connect to each other in very specific ways, which force RNA molecules to twist and loop into a variety of complicated 3D structures."[9] This places many of the DNA letters that create this RNA into the sequence-specific category.

Consider the diagram in Figure 1 of a non-coding RNA molecule.

About 75% of the RNA letters in this structure are linked to another RNA letter, which can only happen between

See **DNA** *on page 5*

DNA

continued from page 4

specific (complementary) letters. Change these letters and they become unlinked. Some of the RNA letters which are not linked likely have function as well.

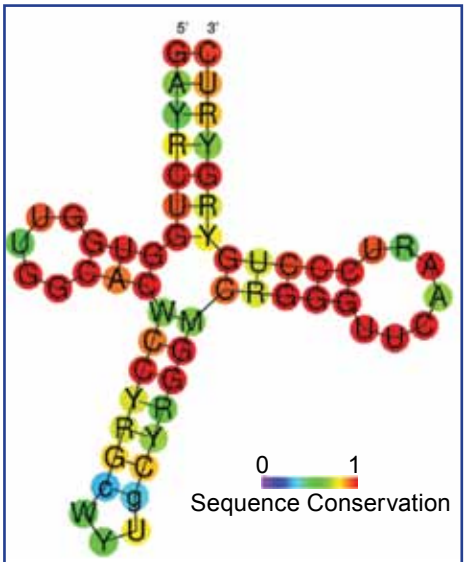

Figure 1. A consensus secondary structure for a ncRNA family called mascRNA-menRNA. Image by Paul Gardner, University of Otago. CC BY-SA 3.0 via Wikimedia Commons.

From exons + protein binding

ENCODE estimated in 2012 that 20% of the genome is made of exons (protein-coding gene regions) or has a specific sequence that proteins use to determine where to latch on to DNA:

> [E]ven with our most conservative estimate of functional elements (8.5% of putative DNA/protein binding regions) and assuming that we have already sampled half of the elements from our transcription factor and cell-type diversity, one would estimate that at a minimum 20% (17% from protein binding and 2.9% protein coding gene exons) of the genome participates in these specific functions, with the likely figure significantly higher.[10]

From what we know of exons and protein binding areas, most of their sequence must be specific. There are, of course, many other types of sequence-specific DNA beyond these categories.

From disease + trait association

A review in 2012 looked at 920 studies involving the genomes of thousands of people.[11] They found that only 4.9% of function-altering mutations occurred within protein-coding DNA.

Another broad research review found only 4% of function-altering mutations (105/2593) were within coding regions.[12] Since only a small percentage of DNA is protein coding (2.9% according to ENCODE above), this implies there's much sequence-specific DNA outside of protein coding regions.

Sequence specific conclusions

The three aforementioned indicators show that we're likely getting many more than 10 mutations that disrupt function per generation. Ten harmful mutations drove the population to extinction in the simulation by Gibson et al.[3] And this is far more than the 1-2 per generation that Larry Moran worries about.[4] This issue caused molecular biologist and anti-creationist Dan Graur to famously proclaim:

> If the human genome is indeed devoid of junk DNA as implied by the ENCODE project, then a long, undirected evolutionary process cannot explain the human genome... If ENCODE is right, evolution is wrong.[13]

If evolution cannot even maintain these large amounts of functional DNA in complex organisms, then it could not have created it.

Common Objections

Evolutionists have not taken these issues lying down. Below are some of the most common objections followed by responses:

"DNA that can be removed is junk"

In 2014 when biologist Craig Venter's team built the first artificial yeast chromosome, they left out or modified 20% of the DNA. The yeast still appeared fine:

> "[T]here are over 50,000 base pairs that were either deleted, inserted or changed in that chromosome of 250,000 base pairs, and it works."[14]

Surely this must mean that DNA is largely junk? Not so. Many genes have functions that are only needed in specific environments. A 2008 study noted than only 20% of yeast genes had an effect when disabled — when the yeast were in a comfortable lab environment. Once they subjected the yeast to various chemical or environmental stresses, they found that 97% of genes had a negative effect when disabled.[15]

Additionally, many genes serve as redundant fallbacks which only kick in when primary systems fail. "Loss-of-function tests can also be buffered by functional redundancy, such that double or triple disruptions are required for a phenotypic consequence."[16]

In *C. elegans* (a simple worm), 89-96% of genes are part of such redundant systems.[17]

"Biochemical activity ≠ function"

Some evolutionists argue that most DNA is copied to RNA randomly and by accident. Therefore, the mere production of RNA does not necessarily indicate that the DNA is functional. However, a 2017 study looked at places where proteins bind to DNA across 75 organisms including humans, mice, fruit flies, and yeast:

> Using in vitro measurements of binding affinities for a large collection of DNA binding proteins, in multiple species, we detect a significant global avoidance of weak binding sites in genomes.[18]

This matters because "Most DNA binding proteins recognize degenerate patterns; i.e., they can bind strongly to tens or hundreds of different possible words and weakly to thousands or more."[18]

If proteins bind to DNA largely at random then we would expect to see mostly weak binding. But we see mostly strong binding. Therefore, most DNA/protein binding indicates function.

See **DNA** *on page 6*

DNA

continued from page 5

As already noted, RNAs being produced at specific times in specific cell types is also evidence they're functional:

> Assertions that the observed transcription represents random noise (tacitly or explicitly justified by reference to stochastic ("noisy") firing of known, legitimate promoters in bacteria and yeast), is more opinion than fact and difficult to reconcile with the exquisite precision of differential cell- and tissue-specific transcription in human cells.[6]

"Less than one transcript per cell"

Among the RNA where ENCODE could estimate its abundance, 70% were detected at levels below "one transcript per cell."[19] ENCODE critics cried foul, claiming that such a small amount of RNA couldn't possibly be doing anything useful.

But the one transcript per cell is just an average. ENCODE studied 147 cell types at various stages of development. If an RNA had 500 copies only in one cell type and at only one stage of development, the average could still be less than one if it wasn't present in any other cell types or developmental stages.

Additionally, an RNA from the HOXA gene (that everyone agrees is functional) was detected at only 0.13 copies per cell. Another functional RNA was found at only "0.0006 transcripts per cell, indicating expression in only a small subpopulation of the cells sampled."[19]

Conclusions

In 1884, long before DNA was discovered, the anti-Christian agnostic Robert G. Ingersoll quipped:

> The church teaches that man was created perfect, and that for six thousand years he has degenerated. Darwin demonstrated the falsity of this dogma. He shows that man has for thousands of ages steadily advanced… that man did not "fall." Charles Darwin destroyed the foundation of orthodox Christianity.[20]

In contrast, over 1800 years earlier the apostle Paul reminded us that all of creation is in bondage to decay:

> For the creation was subjected to futility — not willingly but because of God who subjected it — in hope that the creation itself will also be set free from the bondage of decay into the glorious freedom of God's children. (Romans 8:20-21 NET)

The genomics discoveries of the last two decades have not been kind to Ingersoll, or to Darwin. I eagerly anticipate Christ's return when we'll be freed from this bondage to decay.

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See **DNA** *on page 7*

DNA

continued from page 6

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Summaries

continued from page 3

models have been proposed to explain how the global Flood account in Genesis 6 to 8 may have been responsible for the observed sedimentary rock layers all over the world along with large-scale geological features, such as the Grand Canyon, continental shelves, and the large volume of sediments on the continents. The models also all have a cornerstone assumption that rocks can form on short time scales of months to years rather than over the long time scales of uniformitarian deep time.

In the winter 2024 issue of *CRSQ*, Dunn addresses the need for studies to be conducted to measure the time required for the sediments to compact under pressure, expel fluids, and gradually cement into solid rock—a process called lithification. The paper focuses on the lithification of clay because it tends to hold water and is extremely slow to drain. Soft clays can be up to 90% water and only 10% clay particles by volume (porosity of 0.9), and clay typically does not begin to solidify until its content has reached less than 40-50% water (porosity of 0.4 to 0.5). Dunn gives an example that a 10m-thick layer of clay with a porosity of 0.9 needs to be compacted down to 2m to have a porosity of 0.5. Further compaction occurs as the clay hardens, eventually becoming a 1.33m layer of claystone with a porosity of less than 0.25.

An analogy to a spring is used to explain the three stages of consolidation:

1. A load placed on top is supported by the fluid initially.
2. As water is squeezed out, the weight of the load is gradually transferred from the fluid to the spring.
3. When no more water can be squeezed out, the load is entirely supported by the spring.

A detailed numerical model is presented which is then applied to drilling core data from a borehole drilled in the Labrador Sea off the coast of Greenland. The sediments in the core are dated on the secular time scale as being deposited in the last ten million years. In Flood models, this is either at the end of the Flood or entirely post-Flood. The sediments in the core are a relatively consistent mix of about 40% silt and 60% clay with very little sand, and the porosity decreases with depth from 0.85 at seabed level to 0.4 at depth. Then three scenarios are presented:

1. Flood deposition in 100 days.
2. Post-Flood deposition over the course of 100 years.
3. Slow deposition over standard geological time of nine million years.

There is a limit to how fast the sediment can be deposited. If the water has not escaped up and out quickly enough, the deposition of another layer on top can cause the top layer to fall through. Weak sediment layers can also form submarine landslides in areas where sediment accumulates more than 0.1m/yr.

There are also implications for the formation of trace fossils, such as animal tracks and trackways. These are usually assumed to have formed as animals walked across freshly deposited sediment, but this requires that the sediment be strong enough to support the animals' weight. Silts and clays may be unlikely to develop the necessary strength within the hours-to-days timeframe of the Flood models unless they have a high sand content.

In raising questions about rapid rock formation in Flood models, Dunn suggests this as a topic of experimental scientific study that can help to refine the current understanding of the rock record.

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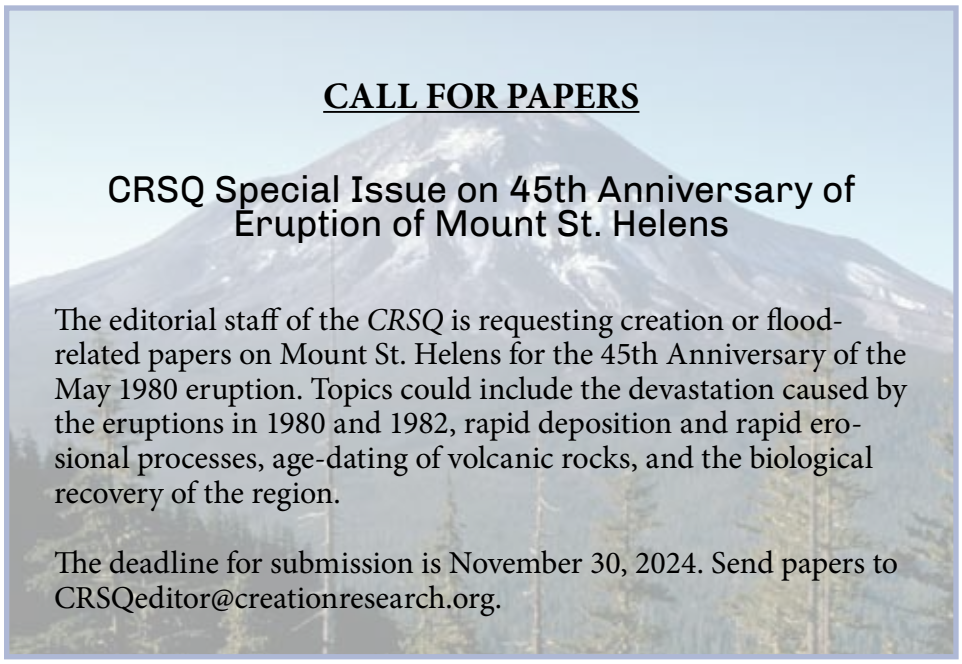

CALL FOR PAPERS

CRSQ Special Issue on 45th Anniversary of Eruption of Mount St. Helens

The editorial staff of the *CRSQ* is requesting creation or flood-related papers on Mount St. Helens for the 45th Anniversary of the May 1980 eruption. Topics could include the devastation caused by the eruptions in 1980 and 1982, rapid deposition and rapid erosional processes, age-dating of volcanic rocks, and the biological recovery of the region.

The deadline for submission is November 30, 2024. Send papers to CRSQeditor@creationresearch.org.

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Prayer Matters

Praise: Thank you for all your prayers and financial support!

We praise God for the birth of a healthy baby girl to our new director and his wife on June 13th. They named her Genesis.

Prayer: Please pray for this year's CRS conference. We want this conference to glorify God, to inform attendees of new advances in creation research, and to be a beneficial time of Christian fellowship. We also pray for safe travel for all those attending.

Please pray for Dr. Joel Brown and family as he moves to Arizona around the first of August to take up his new responsibilities as Director of the Van Andel Creation Research Center and as he teaches classes at Arizona Christian University this fall.

Thanks Again!

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